46

RAW SEQUENCE LISTING PATENT APPLICATION US/08/320,157

DATE: 03/17/95 TIME: 09:29:28

INPUT SET: S2805.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING 1 2 3 General Information: (1) 5 (i) APPLICANT: KIEFER, MICHAEL C. 6 BARR, PHILIP J. 7 8 (ii) TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA 9 ENCODING THE PROTEINS AND METHODS OF USE THEREOF 10 (iii) NUMBER OF SEQUENCES: 22 11 12 (iv) CORRESPONDENCE ADDRESS: 13 14 (A) ADDRESSEE: MORRISON & FOERSTER 15 (B) STREET: 755 Page Mill Road (C) CITY: Palo Alto 16 17 (D) STATE: California 18 (E) COUNTRY: USA 19 (F) ZIP: 94304-1018 20 21 (V) COMPUTER READABLE FORM: 22 (A) MEDIUM TYPE: Floppy disk 23 (B) COMPUTER: IBM PC compatible 24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 26 (vi) CURRENT APPLICATION DATA: 27 (A) APPLICATION NUMBER: US 08/320,157 28 29 (B) FILING DATE: 07-OCT-1994 30 (C) CLASSIFICATION: 31 32 (viii) ATTORNEY/AGENT INFORMATION: (A) NAME: LEHNHARDT, SUSAN K. 33 34 (B) REGISTRATION NUMBER: 33,943 35 (C) REFERENCE/DOCKET NUMBER: 23647-20007.20 36 (ix) TELECOMMUNICATION INFORMATION: 37 38 (A) TELEPHONE: (415) 813-5600 39 (B) TELEFAX: (415) 494-0792 40 (C) TELEX: 706141 41 42 (2) INFORMATION FOR SEQ ID NO:1: 43 44 45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

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INPUT SET: S2805.raw (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: Asp Trp Gly Arg Val Val Ala Ile (2) INFORMATION FOR SEQ ID NO:2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: misc_difference (B) LOCATION: replace(23, "") (D) OTHER INFORMATION: /note= "This position is inosine." (ix) FEATURE: (A) NAME/KEY: misc difference (B) LOCATION: replace(27, "") (D) OTHER INFORMATION: /note= "This position is inosine." (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: AGATCTGAAT TCAACTTGGG GGNCAGNAGT NGTNGC (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: Asp Trp Gly Gly Gln Glu Asn Asp Gln Ile Trp

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1
                           5
                                                10
100
101
102
     (2) INFORMATION FOR SEQ ID NO:4:
103
104
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 29 base pairs
105
106
                (B) TYPE: nucleic acid
107
                (C) STRANDEDNESS: single
108
                (D) TOPOLOGY: linear
109
110
111
          (ix) FEATURE:
112
113
                (A) NAME/KEY: misc difference
114
                (B) LOCATION: replace(6, "")
115
                (D) OTHER INFORMATION: /note= "This position is inosine."
116
          (ix) FEATURE:
117
118
                (A) NAME/KEY: misc_difference
119
                (B) LOCATION: replace(9, "")
                (D) OTHER INFORMATION: /note= "This position is inosine."
120
121
122
123
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
124
                                                                                29
125
     AGGGTNGGNG GNACNAGAGA CATCTAGGT
126
127
     (2) INFORMATION FOR SEQ ID NO:5:
128
           (i) SEQUENCE CHARACTERISTICS:
129
130
                (A) LENGTH: 41 base pairs
131
                (B) TYPE: nucleic acid
132
                (C) STRANDEDNESS: single
133
                (D) TOPOLOGY: linear
134
135
136
          (ix) FEATURE:
137
138
                (A) NAME/KEY: misc difference
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                (B) LOCATION: replace(19, "")
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141
142
          (ix) FEATURE:
143
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144
                (B) LOCATION: replace(22, "")
                (D) OTHER INFORMATION: /note= "This position is inosine."
145
146
147
148
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
149
150
     AGATCTAAGC TTGTCCCANC CNCCNTGNTC CTTGAGATCC A
                                                                                41
151
152
     (2) INFORMATION FOR SEQ ID NO:6:
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/320,157

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153	dia an	011EVAE 41155AEE	TOWTOG	
154	` '	QUENCE CHARACTE		
155 156	•	A) LENGTH: 2094 B) TYPE: nuclei		
	•	•		
157	•	C) STRANDEDNESS	=	
158	(1	D) TOPOLOGY: li	ear	
159				
160				
161	(` m		
162	(ix) FE			
163	•	A) NAME/KEY: CD		
164	(1	B) LOCATION: 20	833	
165				
166			OV	
167	(X1) SEC	QUENCE DESCRIPT	ON: SEQ ID NO:6:	
168				
169	GAGGATCTAC A	AGGGGACAAG TAAA	GCTAC ATCCAGATGC CGGGAATGC	A CTGACGCCCA 60
170				
171	TTCCTGGAAA (CTGGGCTCCC ACTC	GCCCC TGGGAGCAGC AGCCGCCAG	C CCCTCGGACC 120
172				
173	TCCATCTCCA (CCCTGCTGAG CCAC	CGGGT TGGGCCAGGA TCCCGGCAG	G CTGATCCCGT 180
174	aamaa amaa	a.aamama	am maa aaa aaa aaa aaa aa	1 ggm ggg 230
175	CCTCCACTGA (CT TCG GGG CAA GGC CCA GGT	
176			la Ser Gly Gln Gly Pro Gly	
177		1	5	10
178				
179			GCC CTG CCC TCT GCT TCT G	
180	Arg Gin Giu		Ala Leu Pro Ser Ala Ser G	
181		15	20	25
182				mm ma aga 306
183			GTT TTC CGC AGC TAC GTT T	
184	Val Ala Gin	_	Val Phe Arg Ser Tyr Val P	
185		30	35	40
186				100 010 001 274
187			GAA GGG GTG GCT GCC CCT G	
188			Glu Gly Val Ala Ala Pro A	ata Asp Pro
189	45		50 55	
190			all com log log log log	iga ana ama 100
191			CAA CCT AGC AGC ACC ATG	
192			Gln Pro Ser Ser Thr Met G	ity Gin vai
193	60	6	70	
194				200 mm and 470
195			GGG GAC GAC ATC AAC CGA C	
196			Gly Asp Asp Ile Asn Arg A	- -
197	75	80	85	90
198				
199			CAG CAC CTG CAG CCC ACG G	
200	Ser Glu Phe		Gln His Leu Gln Pro Thr A	
201		95	100	105
202				11.0 1.0m 000 =
203			ATT GCC ACC AGC CTG TTT G	
204	Ala Tyr Glu		Ile Ala Thr Ser Leu Phe G	
205		110	115	.20

RAW SEQUENCE LISTING PATENT APPLICATION US/08/320,157

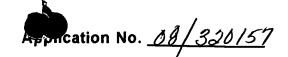
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205	л ш С	חגג	шаа	aaa	COM	OTT C	ama.	CCT	cmm	ana	aaa	መመረ	aaa	መአሮ	ССТ	CTG	614
-																	614
208	тте	Asn	_	Gly	Arg	vaı	vaı		Leu	Leu	GTA	Pne	_	Tyr	Arg	Leu	
209			125					130					135				
210																	
211	GCC	CTA	CAC	GTC	TAC	CAG	CAT	GGC	CTG	ACT	GGC	TTC	CTA	GGC	CAG	GTG	662
212	Ala	Leu	His	Val	Tyr	Gln	His	Gly	Leu	Thr	Gly	Phe	Leu	Cly	Gln	Val	
213		140			_		145					150					
214																	
215	ACC	CGC	TTC	GTG	GTC	GAC	TTC	ATG	CTG	CAT	CAC	TGC	ATT	GCC	CGG	TGG	710
216				Val													, _ •
217	155	9	1110	* 4 4 4	* 41	160			200		165	0,5			9	170	
218	133					100					105					170	
	» mm	a a.	a.a	* 00	aam	000	maa	ama	003	aaa	ama	330	mma	aaa	330	aam	750
219				AGG													758
220	TTE	А⊥а	GIn	Arg	_	GTA	Trp	var	Ата		Leu	Asn	Leu	GIY		GTA	
221					175					180					185		
222																	
223				AAC													806
224	Pro	Ile	Leu	Asn	Val	Leu	Val	Val	Leu	Gly	Val	Val	Leu	Leu	Gly	Gln	
225				190					195					200			
226																	
227	ттт	GTG	GTA	CGA	AGA	TTC	TTC	AAA	TCA	TGA	CTCC	CAA (GGT	GCCC'	гт		853
228				Arq													
229	1110	• • •	205	9	9	1 110		210									
230			203					210									
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231	TGGC	rece	. DDC	FFCAC	JACCC	C TO	SCCT	GAC.	I TA	IGCG!	AAGT	CTT	rGCC.	IIC .	ICIG.	TTCCCT	313
232				aaaa								ama.			aamma		07.2
233	TGC	AGGG.	ree (Jece.	CAAC	JA G	PACAC	JAAGU	J TT	AGC	AAG'I	GTGC	CACT	JCA (GC.II.C	CGGAGG	973
234																	
235	CCC	rgcg:	rgg (GGGC	CAGTO	CA GO	3CTG(CAGA	G GC	ACCTO	CAAC	ATTC	CAT	GT (GCTA	GTGCCC	1033
236																	
237	TCTC	CTCT	GGG (CCCA	GGC'	rg To	GCCC	STCTO	CTC	CCCT	CAGC	TCT	CTGG	GAC (CTCC	TTAGCC	1093
238																	
239	CTGT	CTG	CTA (GGCG	CTGG	G A	BACTO	ATA	A CT	rggg	BAGG	CAAC	GAGA	CTG (GGAG	CCACTT	1153
240																	
241	CTCC	CCA	GAA A	AGTG	TTTA <i>l</i>	AC G	GTTT!	'AGC'	r TT:	TAT	ATA	CCC	TGT	GAG A	AGCC	CATTCC	1213
242																	
243	CACC	CATTO	CTA (CCTG	AGGC	CA GO	GACG'	CTG	GG'	GTG	GGA	TTG	STGG	GTC :	ratg:	rtcccc	1273
244																	
245	AGGZ	ነጥጥር ነ	AGC '	יייי ע יי	тест	A G	ነጥሮ ልር	CACC	י כידי	AGAG	באתמ	GGAG	TTAGG	TAC (CTGAC	CCTGG	1333
246	AUGI	11102	100	.AII	.1001	in Oi	11 CA	CAC		inon	JAIO	COA	INO	JAC (O I OA	300100	1000
247	maan	naaa	7.0m /	700m;		· m ar	пата	7020		,,,,,,,,	аат	N CITE		380 (2000	700220	1393
	TCC	reect	JGT (CCT	AAGCA	AT G	rGTCC	CAG	AGG	AGG	ACC T	ACTA	AGGA	JAG (GCCAAG	1393
248																	
249	GTCC	JTGC'	rca i	ACTCT	rACC(C TO	CTCC:	CAT	r CC!	.ccc1	rccg	GCCI	ATAC'	rgc (CTTT(GCAGTT	1453
250																	
251	GGAC	CTCTC	CAG	GGATT	CTGC	G C	rtggc	GTGT	r ggo	GTG	GGT	GGA	GTCG(CAG A	ACCA	GAGCTG	1513
252																	
253	TCTC	BAAC!	CA (CGTGT	rcag <i>i</i>	AA G	CCTCC	CAAGO	CTC	CCTC	CCCA	AGG	CCT	CTC A	AGTT(CTCTCC	1573
254																	
255	amma	יכייים	יכידי מ	сстти	TAG	C A	CTTG	CTCC	AAC	CCAT	TCA	CTAC	CAGG	rga A	AGGC!	CTCAC	1633
	CTTC	- L L C															
256	CTTC																
256							BAGTO	GCCT	r gci	'AAGC	CTC		CTTGO	CCC 1	AGACT	PACAGG	1693
							SAGTO	GCCT	r GC1	AAGO	SCTC		CTTGC	ccc 1	AGACT	FACAG G	1693







NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s): 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990. 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c). A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e). 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing." 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d). 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e). 7. Other: -

Applicant must provide:

V	An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
4	An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
	A statement that the content of the paper and computer readable copies are the same and, where applicable, include no

For questions regarding compliance with these requirements, please contact:

new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For Patentin software help, call (703) 308-6856

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